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SD5 Light Chain

1 AspIleMetMetSerGlnSerProSerSerLeuThrValSerValGlyGluLysValThrValSerCysLys
 1 GACATTATGATGTCCAGTCTCCATCTCCCTAACTGTGTCTAGTTGGAGAGAGGTACTGTGTGAGCTGCAAG
 25 SerSerGlnSerLeuLeuTyrThrSerSerGlnLysAsnTyrLeuAlaTyrTyrGlnGlnLysProGlyGln
 73 TCCAGTCAGTCCCTTTTATATACTAGCAGTCAGAGAACTACTTGGCTGGTACCAGCAGAAACCAGGTGAG
 49 SerProLysLeuLeuIleTyrTrpAlaSerThrArgGluSerGlyValProAspArgPheThrGlySerGly
 145 TCTCCTAACTGCTGATTTACTGGGCATCCACTAGGGAATCTGGGGTCCCTGATCGCTTCACAGGCAGTGA
 73 SerGlyThrAspPheThrLeuThrIleThrSerValLysAlaAspAspLeuAlaValTyrTyrCysGlnGln
 217 TCTGGGACAGATTTTCACTCTCACCATCACCAGTGTGAAGCTGACGACCTGGCAGTTTATTACTGTGAGCAA
 97 TyrTyrAlaTyrProTrpThrPheGlyGlyGlyThrLysLeuGluIleLysArgThrValAlaAlaProSer
 289 TATTATGCCCTATCCGTGGACGTTCCGTGGAGGCACAAAGTTGGAGATCAACGGACCCGTGGCTGCACCATCT
 121 ValPheIlePheProProSerAspGluGlnLeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsn
 361 GTCTTCATCTTCCCGCCATCTGATGACGAGTGAATCTGGAACCTGCCTCTGTGTGTGCTGCTGAATAAC
 145 PheTyrProArgGluAlaLysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSer
 433 TTCTATCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCATCGGGTAACTCCCGGAGAGT
 169 ValThrGluGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAlaAspTyr
 505 GTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCCTGACCGCTGAGCAAGCAGACTAC
 193 GluLysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerProValThrLysSerPheAsn
 577 GAGAAACACAAAGTCTACGCCCTGGAGAGTCAACCCATCAGGGCCTGAGCTGCCCGCTCACAAGCAGCTTCAAC
 217 ArgGlyGluCys
 649 AGGGGAGAGTGT

FIG. 1A

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5D5 Heavy Chain

1 GlxValGlnLeuGlnInSerGlyProGluLeuValArgProGlyAlaSerValLysMetSerCysArgAla
 1 SAGGTTGAGCTGCAGCAGTCTGGGCCTGAACCTGGTGGGCTTCAGTGAAATGTCCCTGCAGGGCT
 25 SerGlyTyrThrPheThrSerTyrTrpLeuHisTrpValLysGlnArgProGlyProGlyLeuGluTrpIle
 73 TCGGGCTATACCTTCACAGCTACTGGTTGCACTGGGTTAAACAGAGGCCTGGACAGGCCCTTGAGTGGATT
 49 GlyMetIleAspProSerAsnSerAspThrArgPheAsnProAsnPheLysAspLysAlaThrLeuAsnVal
 145 GGCATGATGATCCCTTCCAATAGTGACACTAGGTTTAATCCGAACCTCAAGGACAAGGCCACATTGAATGTA
 73 AspArgSerSerAsnThrAlaTyrMetLeuLeuSerSerLeuThrSerAlaAspSerAlaValTyrTyrCys
 217 GACAGATCTTCCAACACACAGCCCTACATGCTGCTCAGCAGCCTGACATCTGCTGACTCTGCAGTCTATTACTGT
 97 AlaThrTyrGlySerTyrValSerProLeuAspTyrTrpGlyGlnGlyThrSerValThrValSerSerAla
 289 GCCACATATGGTAGCTACGTTTCCCTCTGGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTTCCGCC
 121 SerThrLysGlyProSerValPheProLeuAlaProSerSerLysSerThrSerGlyGlyThrAlaAlaLeu
 361 TCCACCAAGGGCCCATCGGTCTTCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTG
 145 GlyCysLeuValLysAspTyrPheProGluProValThrValSerTrpAsnSerGlyAlaLeuThrSerGly
 433 GGCTGCCCTGGTCAAGGACTACTTCCCGAACCCTGACGGTGTCTGGTGAACCTCAGGGGCCCTGACCGCGGC
 169 ValHisThrPheProAlaValLeuGlnSerSerGlyLeuTyrSerLeuSerSerValValThrValProSer
 505 GTGCACACCTTCCCGGCTGTCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGGTGGTGACCCGTGCCCTCC
 193 SerSerLeuGlyThrGlnThrTyrIleCysAsnValAsnHisLysProSerAsnThrLysValAspLysLys
 577 AGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAAGCCACACCAAGGTCGACAAAGAA
 217 ValGluProLysSerCysAspLysThrHisThrAlaAlaPro
 649 GTTGAGCCCCAAATCTTGTGACAAACTCACACAGCTGCGCCG

FIG. 1B

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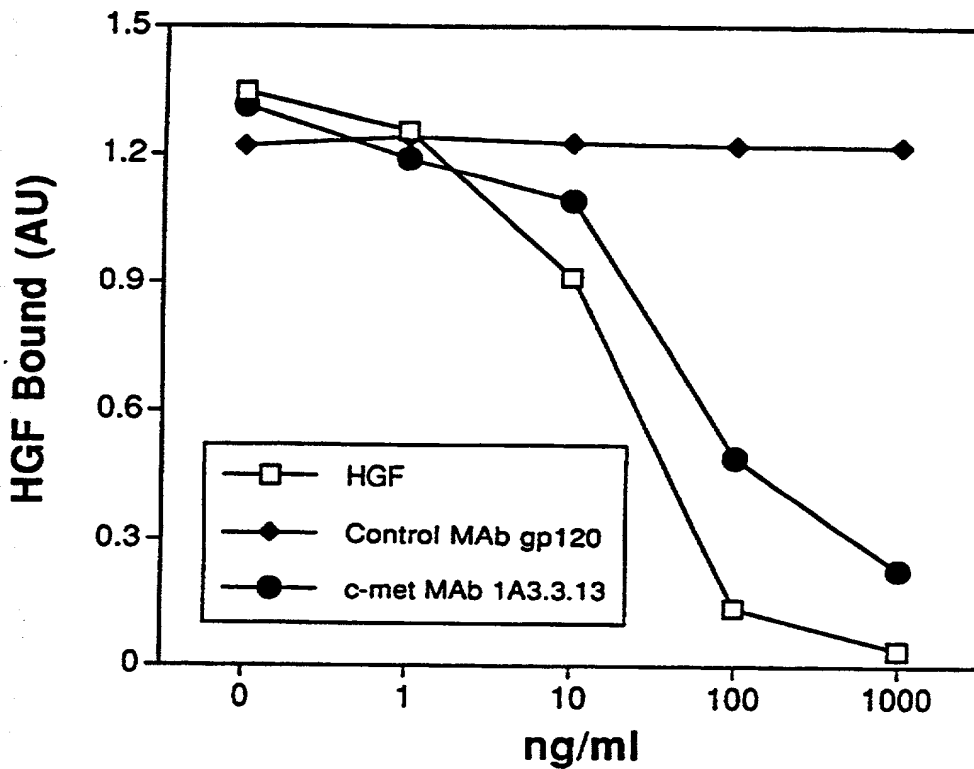


FIG. 2

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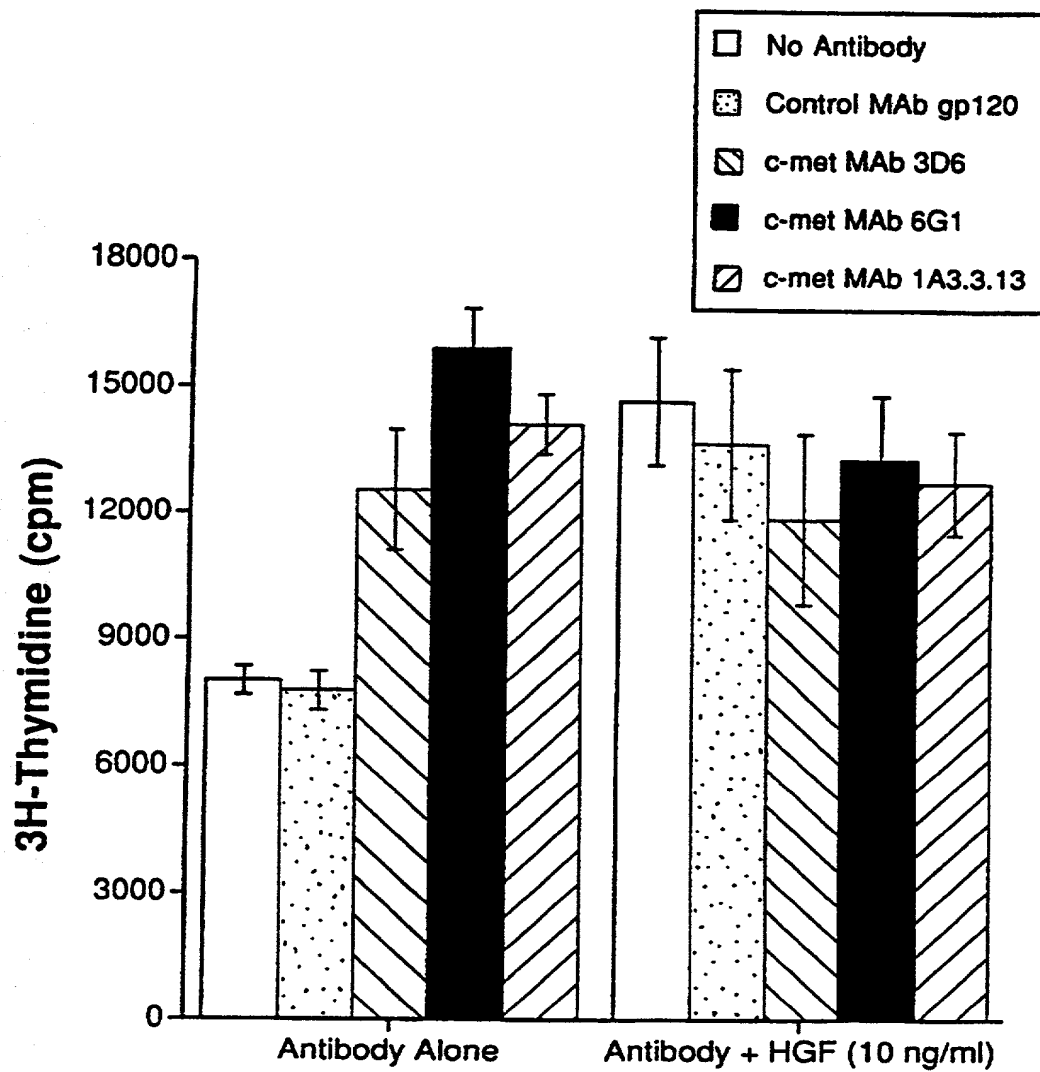


FIG. 3

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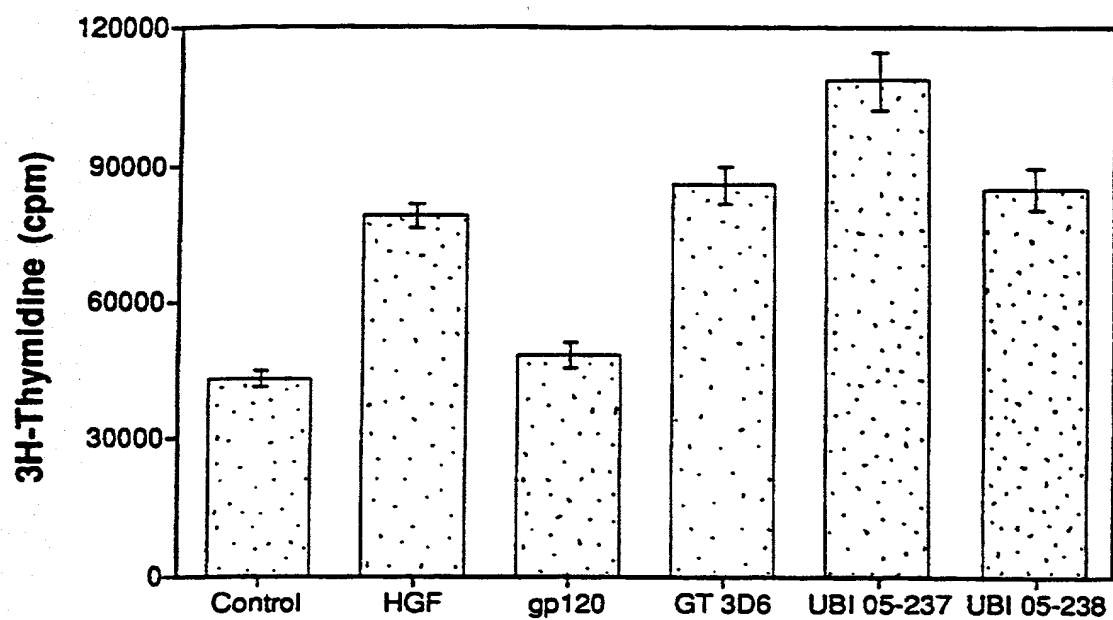


FIG. 4

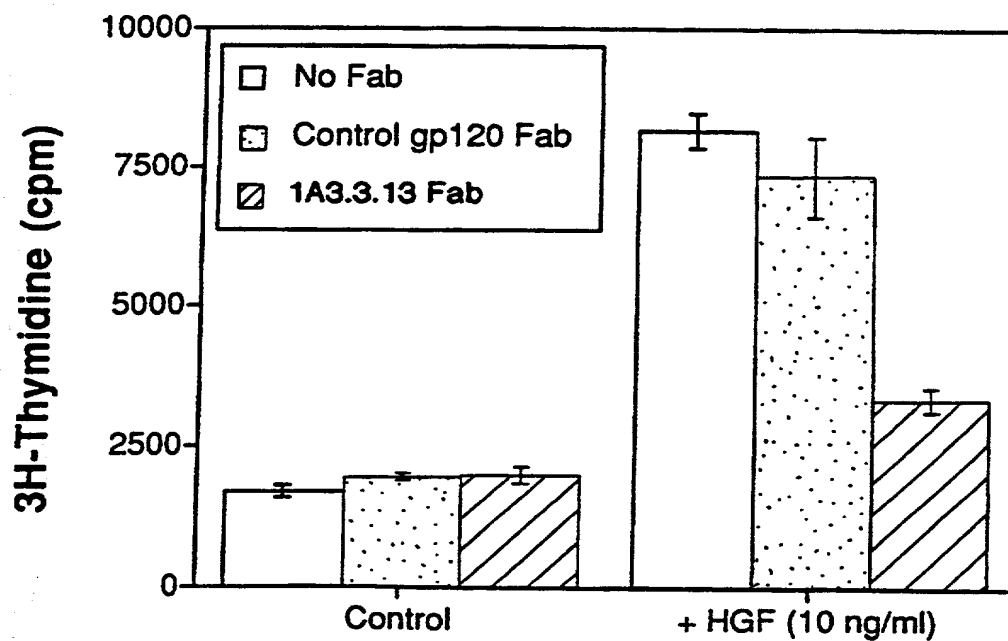
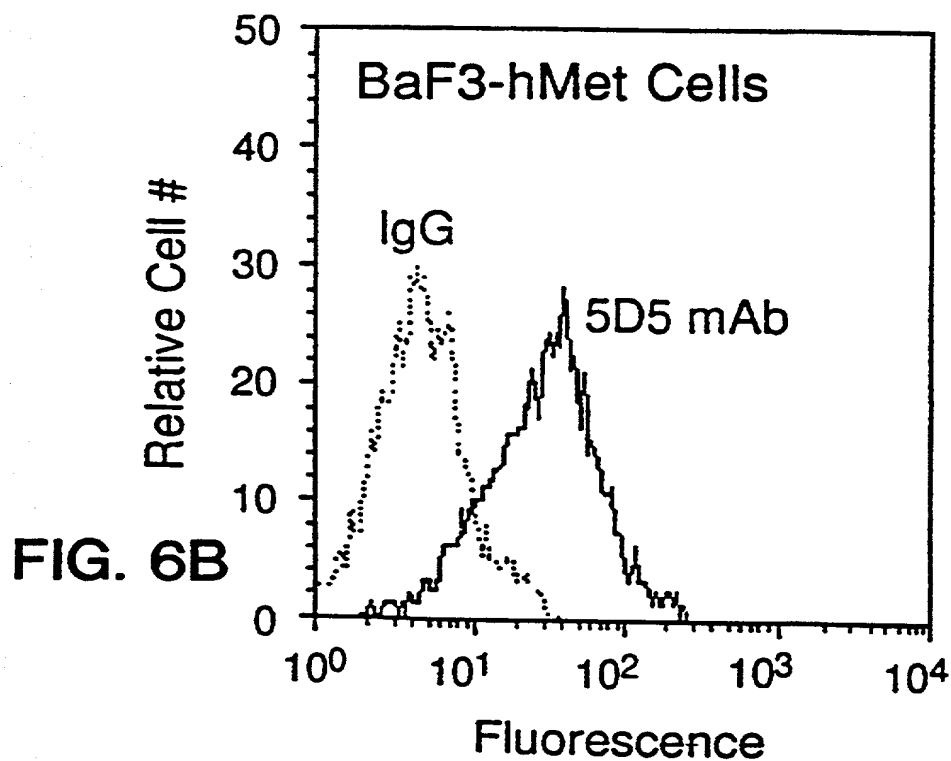
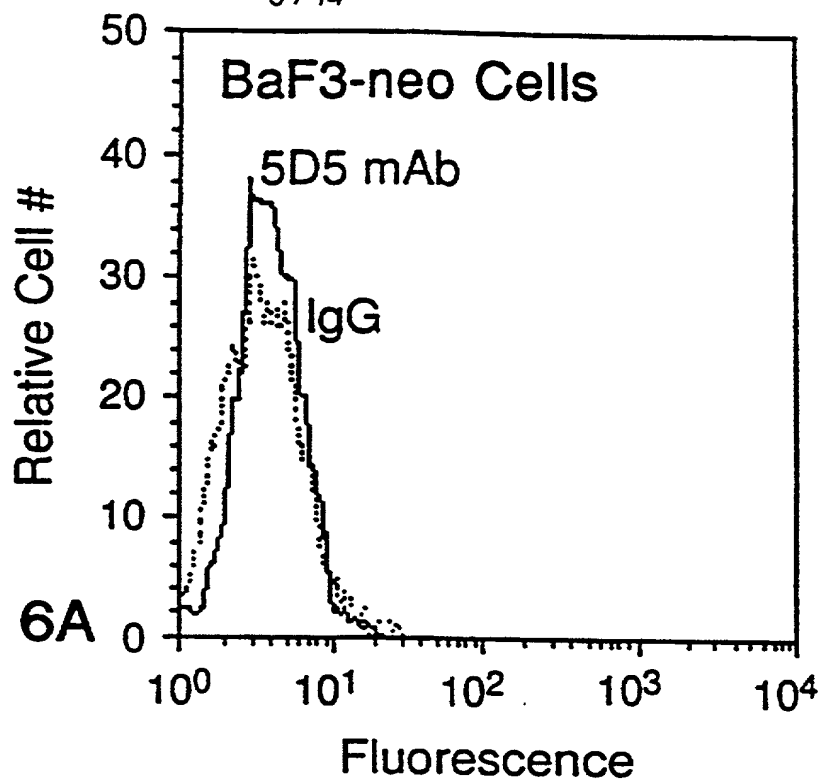


FIG. 5

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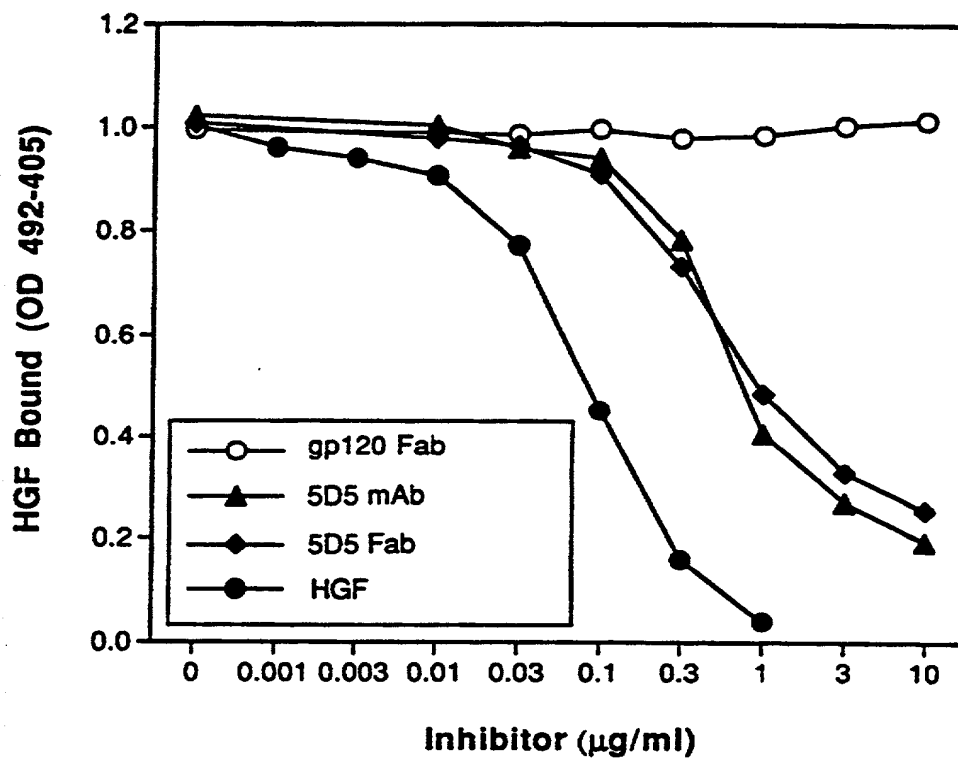
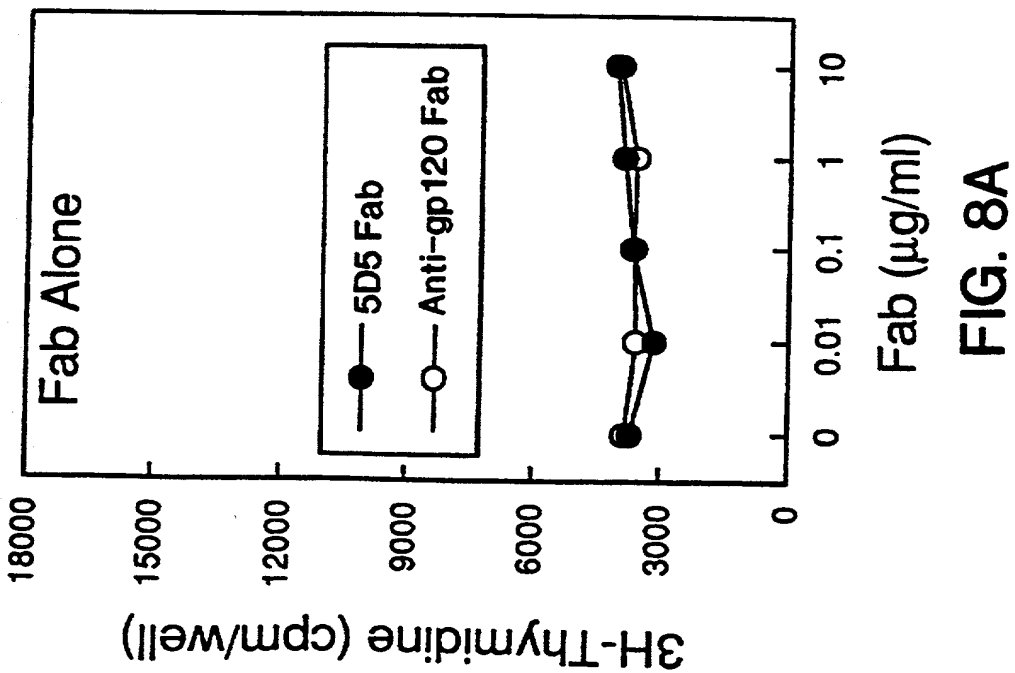
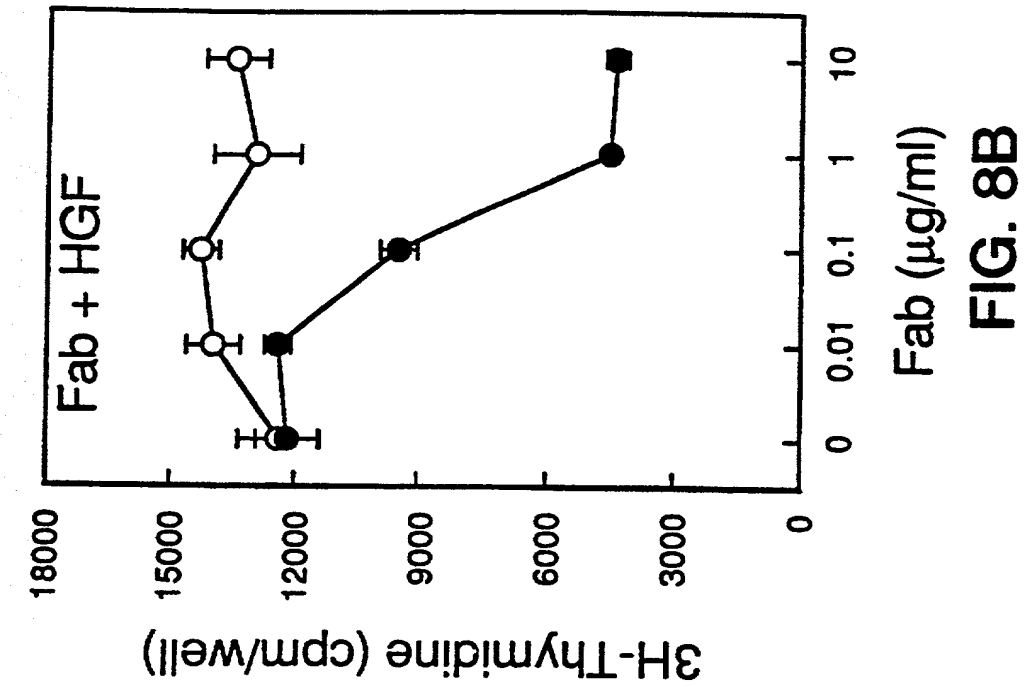


FIG. 7

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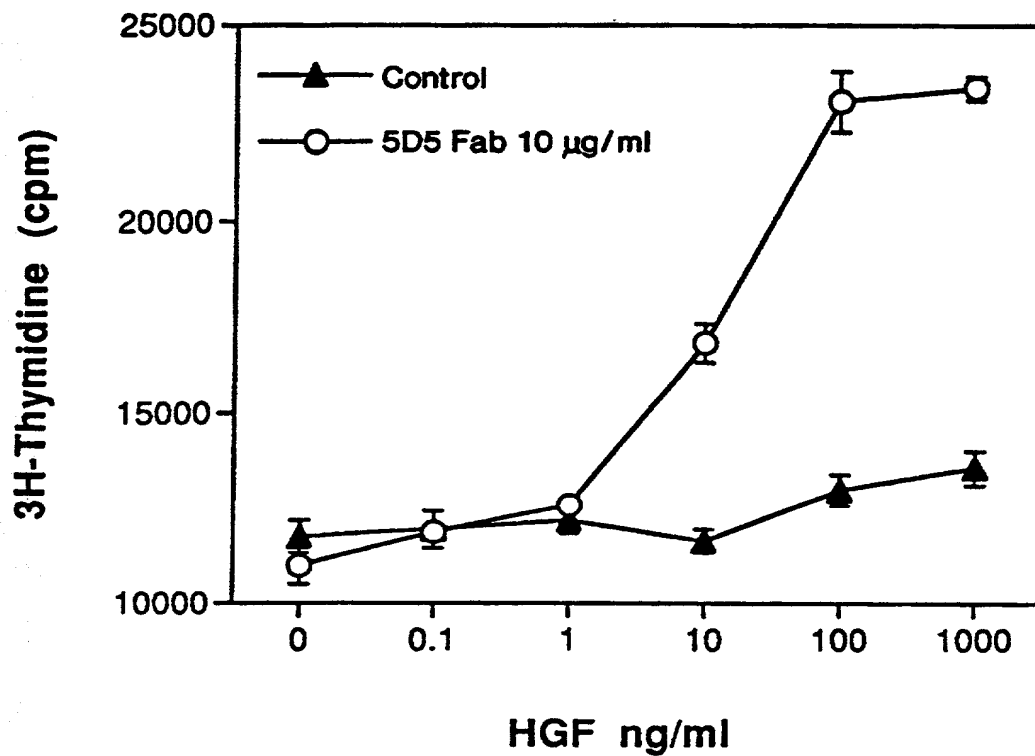
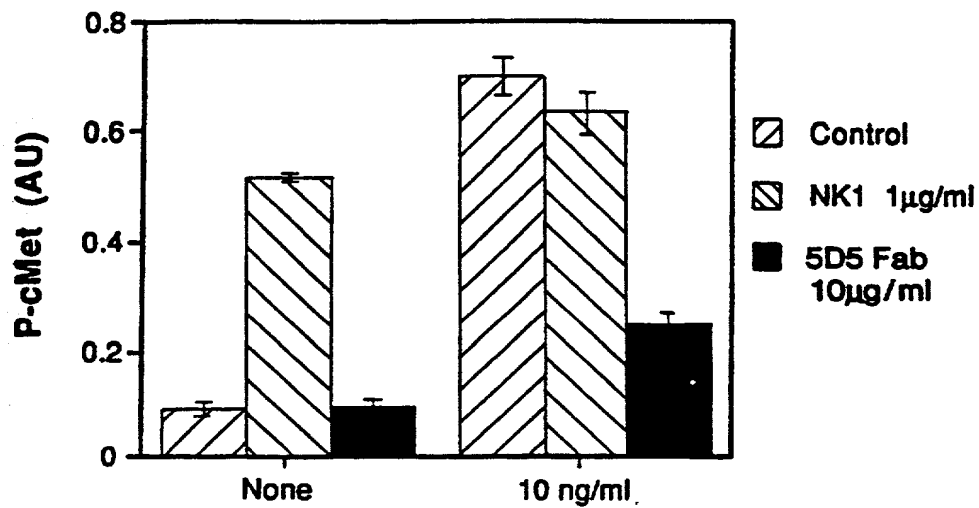


FIG. 9

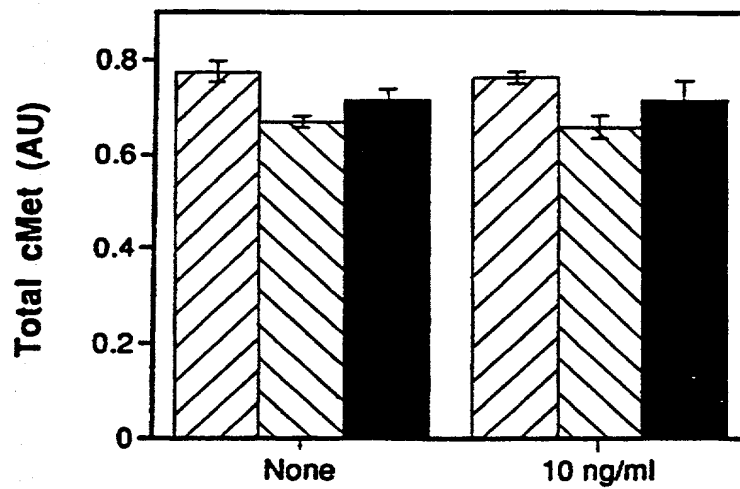
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HGF

FIG. 10A



HGF

FIG. 10B

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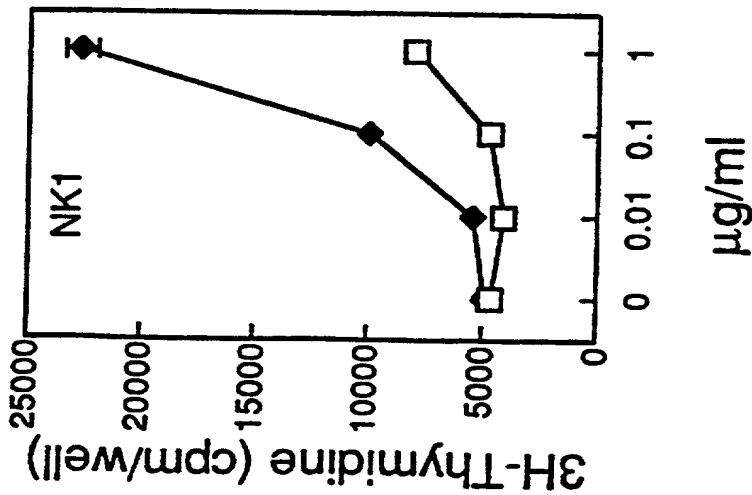


FIG. 11A

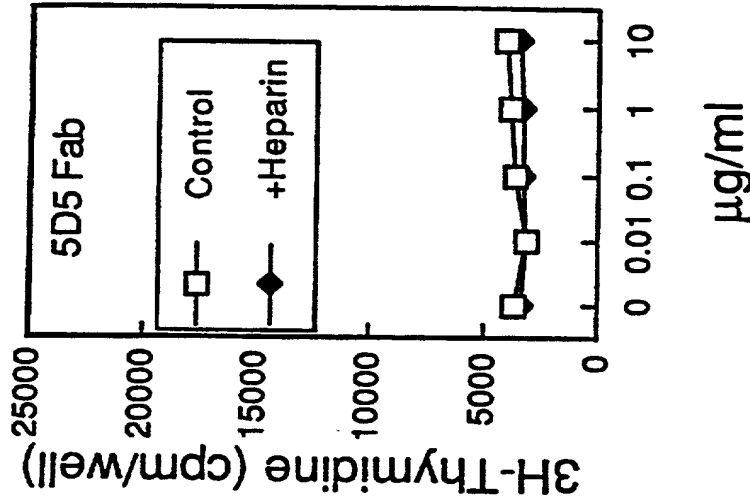


FIG. 11B

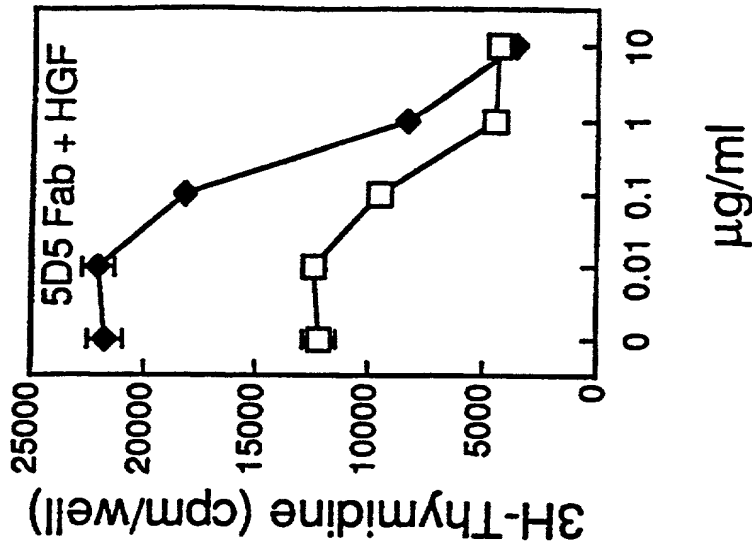


FIG. 11C

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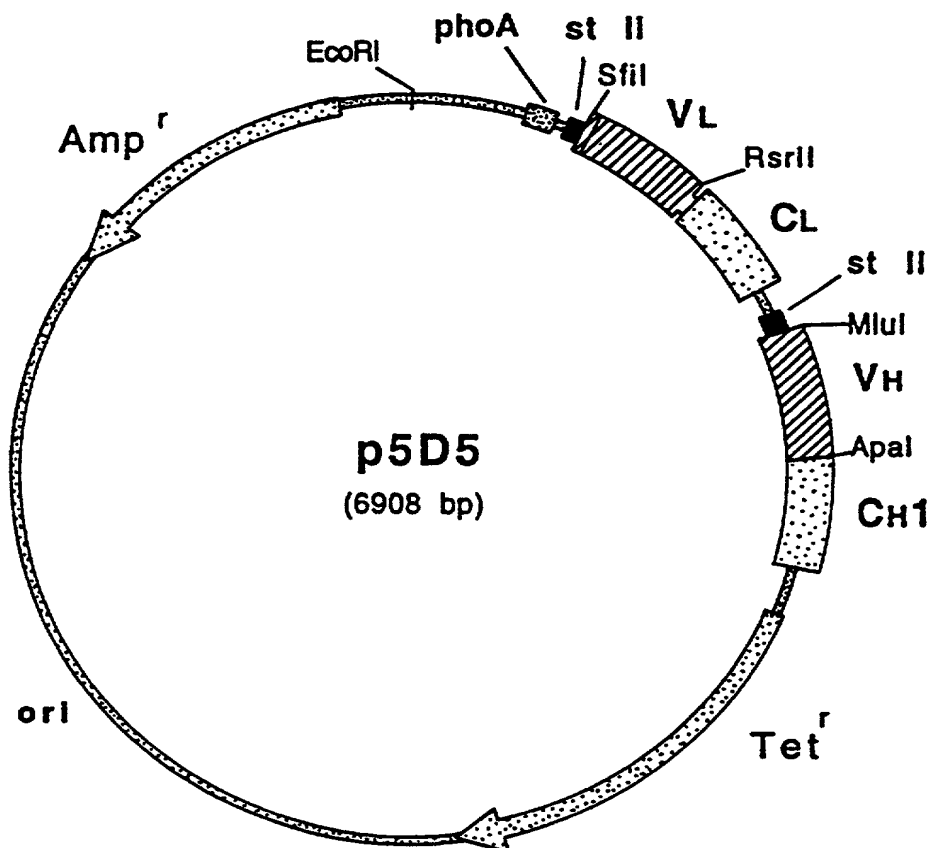


FIG. 12

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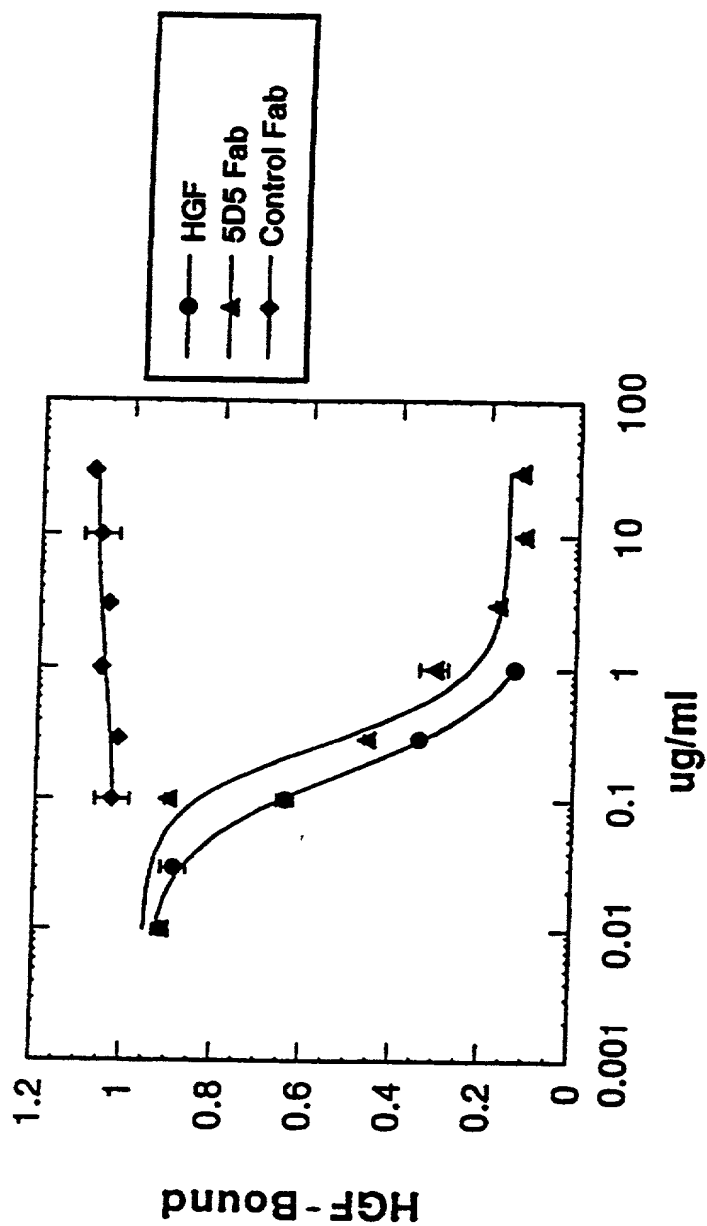


FIG. 13

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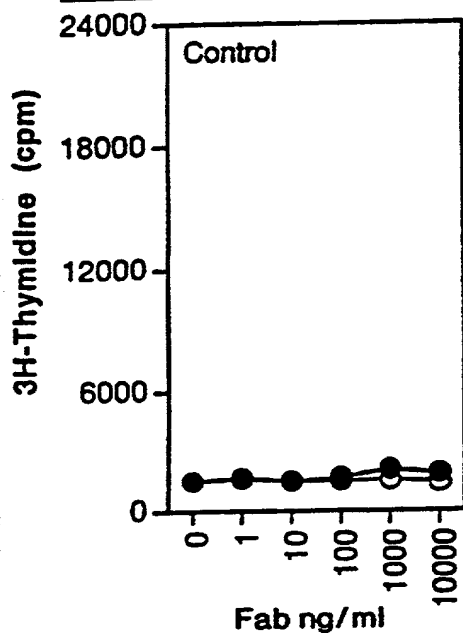
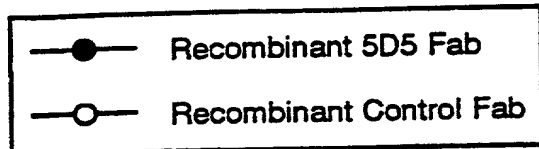


FIG. 14A

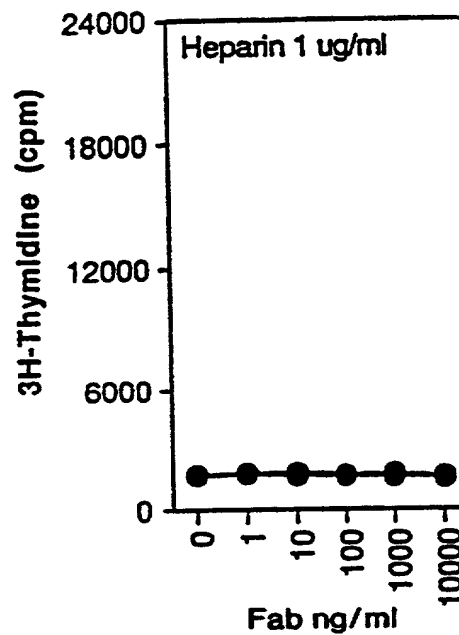


FIG. 14B

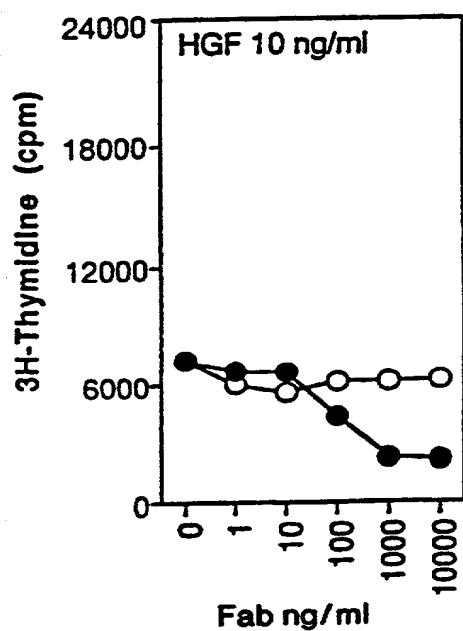


FIG. 14C

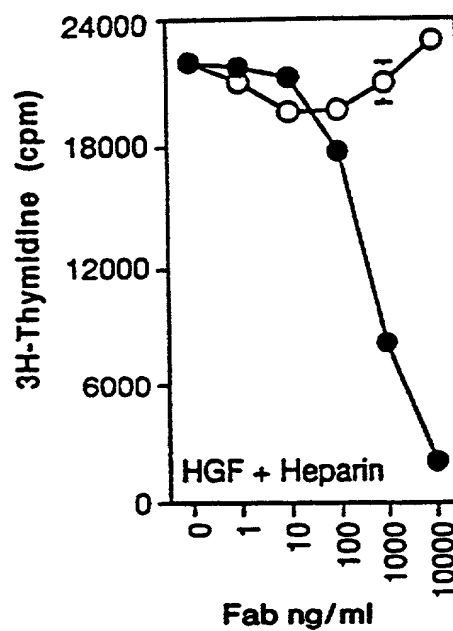


FIG. 14D

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